

Mark E Bowen

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

1,275
citations

567144

15
h-index

752573

20
g-index

23
all docs

23
docs citations

23
times ranked

1970
citing authors

#	ARTICLE	IF	CITATIONS
1	Precision and accuracy of single-molecule FRET measurements—a multi-laboratory benchmark study. <i>Nature Methods</i> , 2018, 15, 669-676.	9.0	350
2	Accessory Proteins Stabilize the Acceptor Complex for Synaptobrevin, the 1:1 Syntaxin/SNAP-25 Complex. <i>Structure</i> , 2008, 16, 308-320.	1.6	151
3	Beyond the Random Coil: Stochastic Conformational Switching in Intrinsically Disordered Proteins. <i>Structure</i> , 2011, 19, 566-576.	1.6	109
4	Optimizing Methods to Recover Absolute FRET Efficiency from Immobilized Single Molecules. <i>Biophysical Journal</i> , 2010, 99, 961-970.	0.2	93
5	Supertertiary structure of the synaptic MAGuK scaffold proteins is conserved. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15775-15780.	3.3	66
6	The insulin and IGF1 receptor kinase domains are functional dimers in the activated state. <i>Nature Communications</i> , 2015, 6, 6406.	5.8	60
7	Structure of the full-length <i>Clostridium difficile</i> toxin B. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 712-719.	3.6	59
8	Effect of Src Kinase Phosphorylation on Disordered C-terminal Domain of N-Methyl-d-aspartic Acid (NMDA) Receptor Subunit GluN2B Protein. <i>Journal of Biological Chemistry</i> , 2011, 286, 29904-29912.	1.6	44
9	Domain Orientation in the N-Terminal PDZ Tandem from PSD-95 Is Maintained in the Full-Length Protein. <i>Structure</i> , 2011, 19, 810-820.	1.6	41
10	Divergent roles of a peripheral transmembrane segment in AMPA and NMDA receptors. <i>Journal of General Physiology</i> , 2017, 149, 661-680.	0.9	41
11	Identifying weak interdomain interactions that stabilize the supertertiary structure of the N-terminal tandem PDZ domains of PSD-95. <i>Nature Communications</i> , 2018, 9, 3724.	5.8	41
12	Spontaneous Switching among Conformational Ensembles in Intrinsically Disordered Proteins. <i>Biomolecules</i> , 2019, 9, 114.	1.8	41
13	Site-Specific Phosphorylation of PSD-95 PDZ Domains Reveals Fine-Tuned Regulation of Protein-Protein Interactions. <i>ACS Chemical Biology</i> , 2017, 12, 2313-2323.	1.6	40
14	Modulating the Intrinsic Disorder in the Cytoplasmic Domain Alters the Biological Activity of the N-Methyl-d-aspartate-sensitive Glutamate Receptor. <i>Journal of Biological Chemistry</i> , 2013, 288, 22506-22515.	1.6	33
15	A viral-fusion-peptide-like molecular switch drives membrane insertion of botulinum neurotoxin A1. <i>Nature Communications</i> , 2018, 9, 5367.	5.8	30
16	Immobilization of Proteins for Single-Molecule Fluorescence Resonance Energy Transfer Measurements of Conformation and Dynamics. , 2012, 896, 3-20.		26
17	Probing Interdomain Linkers and Protein Supertertiary Structure In Vitro and in Live Cells with Fluorescent Protein Resonance Energy Transfer. <i>Journal of Molecular Biology</i> , 2021, 433, 166793.	2.0	17
18	Reconstitution of Multivalent PDZ Domain Binding to the Scaffold Protein PSD-95 Reveals Ternary-Complex Specificity of Combinatorial Inhibition. <i>Structure</i> , 2014, 22, 1458-1466.	1.6	15

#	ARTICLE	IF	CITATIONS
19	Structure and conformational dynamics of <i>Clostridioides difficile</i> toxin A. Life Science Alliance, 2022, 5, e202201383.	1.3	8
20	Conformational change of Syntaxin-3b in regulating SNARE complex assembly in the ribbon synapses. Scientific Reports, 2022, 12, .	1.6	2